

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 7,288,390 B2
APPLICATION NO. : 09/920267
DATED : October 30, 2007
INVENTOR(S) : Heavner et al.

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It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 69, line 20 to Column 79, line 18: cancel the Sequence Listing beginning with
“(1) GENERAL INFORMATION:” and ending with “Leu” in column 79, line 18, and
insert the following Sequence Listing:

Signed and Sealed this
Fourth Day of January, 2011

A handwritten signature in black ink that reads "David J. Kappos". The signature is written in a cursive, flowing style with a large initial "D" and a stylized "K".

David J. Kappos
Director of the United States Patent and Trademark Office

--

SEQUENCE LISTING

<110> Centocor, Inc.
Giles-Komar, Jill
Tripathi, Mohit
Snyder, Linda
Nakada, Marian

<120> ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES

<130> CEN 249

<140> US 09/920,267

<141> 2001-08-01

<150> 60/223,363

<151> 2000-08-07

<160> 17

<170> PatentIn version 3.1

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<212> PRT

<213> Homo sapiens

<400> 2

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1 5 10 15

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<211> 10

<212> PRT

<213> Homo sapiens

<400> 3

Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile
1 5 10

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<210> 4
<211> 11
<212> PRT
<213> Homo sapiens

<400> 4

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 5
<211> 7
<212> PRT
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1 5

<210> 7
<211> 119
<212> PRT
<213> Homo sapiens

<400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Arg Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Phe Asp Gly Ser Asn Lys Tyr Tyr Val Asp Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr
65 70 75 80

Leu Gln Val Asn Ile Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Ala Arg Gly Ser Tyr Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 8
<211> 108
<212> PRT
<213> Homo sapiens

<400> 8

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 9
<211> 1048
<212> PRT
<213> Homo sapiens

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<400> 9

Met Ala Phe Pro Pro Arg Arg Arg Leu Arg Leu Gly Pro Arg Gly Leu
1 5 10 15

Pro Leu Leu Leu Ser Gly Leu Leu Leu Pro Leu Cys Arg Ala Phe Asn
20 25 30

Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
35 40 45

Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
50 55 60

Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
65 70 75 80

Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
85 90 95

Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
100 105 110

Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
115 120 125

Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
130 135 140

Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu
145 150 155 160

Gln Asp Gly Thr Lys Thr Val Glu Tyr Ala Pro Cys Arg Ser Gln Asp
165 170 175

Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Gly Phe Ser Ile Asp
180 185 190

Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr
195 200 205

Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys
210 215 220

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Tyr Asp Pro Asn Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr
225 230 235 240

Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val
245 250 255

Ala Val Gly Asp Phe Asn Gly Asp Gly Ile Asp Asp Phe Val Ser Gly
260 265 270

Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly
275 280 285

Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Met Ala Ala
290 295 300

Tyr Phe Gly Phe Ser Val Ala Ala Thr Asp Ile Asn Gly Asp Asp Tyr
305 310 315 320

Ala Asp Val Phe Ile Gly Ala Pro Leu Phe Met Asp Arg Gly Ser Asp
325 330 335

Gly Lys Leu Gln Glu Val Gly Gln Val Ser Val Ser Leu Gln Arg Ala
340 345 350

Ser Gly Asp Phe Gln Thr Thr Lys Leu Asn Gly Phe Glu Val Phe Ala
355 360 365

Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Gln Asp Gly
370 375 380

Phe Asn Asp Ile Ala Ile Ala Ala Pro Tyr Gly Gly Glu Asp Lys Lys
385 390 395 400

Gly Ile Val Tyr Ile Phe Asn Gly Arg Ser Thr Gly Leu Asn Ala Val
405 410 415

Pro Ser Gln Ile Leu Glu Gly Gln Trp Ala Ala Arg Ser Met Pro Pro
420 425 430

Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly
435 440 445

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Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu
450 455 460

Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr
465 470 475 480

Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr
485 490 495

Ala Leu Lys Val Ser Cys Phe Asn Val Arg Phe Cys Leu Lys Ala Asp
500 505 510

Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu
515 520 525

Leu Asp Lys Leu Lys Gln Lys Gly Ala Ile Arg Arg Ala Leu Phe Leu
530 535 540

Tyr Ser Arg Ser Pro Ser His Ser Lys Asn Met Thr Ile Ser Arg Gly
545 550 555 560

Gly Leu Met Gln Cys Glu Glu Leu Ile Ala Tyr Leu Arg Asp Glu Ser
565 570 575

Glu Phe Arg Asp Lys Leu Thr Pro Ile Thr Ile Phe Met Glu Tyr Arg
580 585 590

Leu Asp Tyr Arg Thr Ala Ala Asp Thr Thr Gly Leu Gln Pro Ile Leu
595 600 605

Asn Gln Phe Thr Pro Ala Asn Ile Ser Arg Gln Ala His Ile Leu Leu
610 615 620

Asp Cys Gly Glu Asp Asn Val Cys Lys Pro Lys Leu Glu Val Ser Val
625 630 635 640

Asp Ser Asp Gln Lys Lys Ile Tyr Ile Gly Asp Asp Asn Pro Leu Thr
645 650 655

Leu Ile Val Lys Ala Gln Asn Gln Gly Glu Gly Ala Tyr Glu Ala Glu
660 665 670

Leu Ile Val Ser Ile Pro Leu Gln Ala Asp Phe Ile Gly Val Val Arg

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675					680					685					
Asn	Asn	Glu	Ala	Leu	Ala	Arg	Leu	Ser	Cys	Ala	Phe	Lys	Thr	Glu	Asn
690						695					700				
Gln	Thr	Arg	Gln	Val	Val	Cys	Asp	Leu	Gly	Asn	Pro	Met	Lys	Ala	Gly
705						710					715				720
Thr	Gln	Leu	Leu	Ala	Gly	Leu	Arg	Phe	Ser	Val	His	Gln	Gln	Ser	Glu
				725					730					735	
Met	Asp	Thr	Ser	Val	Lys	Phe	Asp	Leu	Gln	Ile	Gln	Ser	Ser	Asn	Leu
			740					745					750		
Phe	Asp	Lys	Val	Ser	Pro	Val	Val	Ser	His	Lys	Val	Asp	Leu	Ala	Val
		755					760					765			
Leu	Ala	Ala	Val	Glu	Ile	Arg	Gly	Val	Ser	Ser	Pro	Asp	His	Ile	Phe
	770					775						780			
Leu	Pro	Ile	Pro	Asn	Trp	Glu	His	Lys	Glu	Asn	Pro	Glu	Thr	Glu	Glu
785						790					795				800
Asp	Val	Gly	Pro	Val	Val	Gln	His	Ile	Tyr	Glu	Leu	Arg	Asn	Asn	Gly
				805					810					815	
Pro	Ser	Ser	Phe	Ser	Lys	Ala	Met	Leu	His	Leu	Gln	Trp	Pro	Tyr	Lys
			820					825					830		
Tyr	Asn	Asn	Asn	Thr	Leu	Leu	Tyr	Ile	Leu	His	Tyr	Asp	Ile	Asp	Gly
	835						840					845			
Pro	Met	Asn	Cys	Thr	Ser	Asp	Met	Glu	Ile	Asn	Pro	Leu	Arg	Ile	Lys
	850					855					860				
Ile	Ser	Ser	Leu	Gln	Thr	Thr	Glu	Lys	Asn	Asp	Thr	Val	Ala	Gly	Gln
865						870					875				880
Gly	Glu	Arg	Asp	His	Leu	Ile	Thr	Lys	Arg	Asp	Leu	Ala	Leu	Ser	Glu
				885					890					895	
Gly	Asp	Ile	His	Thr	Leu	Gly	Cys	Gly	Val	Ala	Gln	Cys	Leu	Lys	Ile
			900					905					910		

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Val Cys Gln Val Gly Arg Leu Asp Arg Gly Lys Ser Ala Ile Leu Tyr
915 920 925

Val Lys Ser Leu Leu Trp Thr Glu Thr Phe Met Asn Lys Glu Asn Gln
930 935 940

Asn His Ser Tyr Ser Leu Lys Ser Ser Ala Ser Phe Asn Val Ile Glu
945 950 955 960

Phe Pro Tyr Lys Asn Leu Pro Ile Glu Asp Ile Thr Asn Ser Thr Leu
965 970 975

Val Thr Thr Asn Val Thr Trp Gly Ile Gln Pro Ala Pro Met Pro Val
980 985 990

Pro Val Trp Val Ile Ile Leu Ala Val Leu Ala Gly Leu Leu Leu Leu
995 1000 1005

Ala Val Leu Val Phe Val Met Tyr Arg Met Gly Phe Phe Lys Arg
1010 1015 1020

Val Arg Pro Pro Gln Glu Glu Gln Glu Arg Glu Gln Leu Gln Pro
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His Glu Asn Gly Glu Gly Asn Ser Glu Thr
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<400> 10
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<211> 30
<212> DNA
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<400> 13
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<400> 14
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<212> DNA
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<212> PRT
<213> Homo sapiens

<400> 16

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Leu Gly Ala Leu Ala Gly Val Gly Val Gly Gly Pro Asn Ile Cys Thr
20 25 30

Thr Arg Gly Val Ser Ser Cys Gln Gln Cys Leu Ala Val Ser Pro Met
35 40 45

Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro Leu Gly Ser Pro Arg Cys
50 55 60

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Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn Cys Ala Pro Glu Ser Ile
65 70 75 80

Glu Phe Pro Val Ser Glu Ala Arg Val Leu Glu Asp Arg Pro Leu Ser
85 90 95

Asp Lys Gly Ser Gly Asp Ser Ser Gln Val Thr Gln Val Ser Pro Gln
100 105 110

Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp Ser Lys Asn Phe Ser Ile
115 120 125

Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile Tyr Tyr Leu Met
130 135 140

Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile Gln Asn Leu
145 150 155 160

Gly Thr Lys Leu Ala Thr Gln Met Arg Lys Leu Thr Ser Asn Leu Arg
165 170 175

Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro Tyr Met Tyr
180 185 190

Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr
195 200 205

Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr Leu Thr Asp
210 215 220

Gln Val Thr Arg Phe Asn Glu Glu Val Lys Lys Gln Ser Val Ser Arg
225 230 235 240

Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr
245 250 255

Val Cys Asp Glu Lys Ile Gly Trp Arg Asn Asp Ala Ser His Leu Leu
260 265 270

Val Phe Thr Thr Asp Ala Lys Thr His Ile Ala Leu Asp Gly Arg Leu
275 280 285

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Ala Gly Ile Val Gln Pro Asn Asp Gly Gln Cys His Val Gly Ser Asp
290 295 300

Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro Ser Leu Gly Leu
305 310 315 320

Met Thr Glu Lys Leu Ser Gln Lys Asn Ile Asn Leu Ile Phe Ala Val
325 330 335

Thr Glu Asn Val Val Asn Leu Tyr Gln Asn Tyr Ser Glu Leu Ile Pro
340 345 350

Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser Ser Asn Val Leu Gln
355 360 365

Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser Lys Val Glu Leu Glu
370 375 380

Val Arg Asp Leu Pro Glu Glu Leu Ser Leu Ser Phe Asn Ala Thr Cys
385 390 395 400

Leu Asn Asn Glu Val Ile Pro Gly Leu Lys Ser Cys Met Gly Leu Lys
405 410 415

Ile Gly Asp Thr Val Ser Phe Ser Ile Glu Ala Lys Val Arg Gly Cys
420 425 430

Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile Lys Pro Val Gly Phe Lys
435 440 445

Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys Gln
450 455 460

Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly Thr
465 470 475 480

Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser Gln
485 490 495

Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu Cys
500 505 510

Ser Pro Arg Glu Gly Gln Pro Val Cys Ser Gln Arg Gly Glu Cys Leu

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515	520	525
Cys Gly Gln Cys Val Cys His Ser Ser Asp Phe Gly Lys Ile Thr Gly		
530	535	540
Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys Val Arg Tyr Lys Gly Glu		
545	550	555
Met Cys Ser Gly His Gly Gln Cys Ser Cys Gly Asp Cys Leu Cys Asp		
	565	570
Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys Thr Thr Arg Thr Asp Thr		
	580	585
Cys Met Ser Ser Asn Gly Leu Leu Cys Ser Gly Arg Gly Lys Cys Glu		
	595	600
Cys Gly Ser Cys Val Cys Ile Gln Pro Gly Ser Tyr Gly Asp Thr Cys		
610	615	620
Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys		
625	630	635
Val Glu Cys Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr		
	645	650
Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys		
	660	665
Asp Thr Gly Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp		
	675	680
Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile		
690	695	700
Leu Tyr Val Val Glu Glu Pro Glu Cys Pro Lys Gly Pro Asp Ile Leu		
705	710	715
Val Val Leu Leu Ser Val Met Gly Ala Ile Leu Leu Ile Gly Leu Ala		
	725	730
Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr Ile His Asp Arg Lys Glu		
	740	745
		750

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Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg Ala Lys Trp Asp Thr Ala
755 760 765

Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr Phe Thr Asn Ile Thr
770 775 780

Tyr Arg Gly Thr
785

<210> 17
<211> 799
<212> PRT
<213> Homo sapiens

<400> 17

Met Pro Arg Ala Pro Ala Pro Leu Tyr Ala Cys Leu Leu Gly Leu Cys
1 5 10 15

Ala Leu Leu Pro Arg Leu Ala Gly Leu Asn Ile Cys Thr Ser Gly Ser
20 25 30

Ala Thr Ser Cys Glu Glu Cys Leu Leu Ile His Pro Lys Cys Ala Trp
35 40 45

Cys Ser Lys Glu Asp Phe Gly Ser Pro Arg Ser Ile Thr Ser Arg Cys
50 55 60

Asp Leu Arg Ala Asn Leu Val Lys Asn Gly Cys Gly Gly Glu Ile Glu
65 70 75 80

Ser Pro Ala Ser Ser Phe His Val Leu Arg Ser Leu Pro Leu Ser Ser
85 90 95

Lys Gly Ser Gly Ser Ala Gly Trp Asp Val Ile Gln Met Thr Pro Gln
100 105 110

Glu Ile Ala Val Asn Leu Arg Pro Gly Asp Lys Thr Thr Phe Gln Leu
115 120 125

Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Leu Tyr Tyr Leu Met
130 135 140

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Asp Leu Ser Leu Ser Met Lys Asp Asp Leu Asp Asn Ile Arg Ser Leu
145 150 155 160

Gly Thr Lys Leu Ala Glu Glu Met Arg Lys Leu Thr Ser Asn Phe Arg
165 170 175

Leu Gly Phe Gly Ser Phe Val Asp Lys Asp Ile Ser Pro Phe Ser Tyr
180 185 190

Thr Ala Pro Arg Tyr Gln Thr Asn Pro Cys Ile Gly Tyr Lys Leu Phe
195 200 205

Pro Asn Cys Val Pro Ser Phe Gly Phe Arg His Leu Leu Pro Leu Thr
210 215 220

Asp Arg Val Asp Ser Phe Asn Glu Glu Val Arg Lys Gln Arg Val Ser
225 230 235 240

Arg Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp Ala Val Leu Gln Ala
245 250 255

Ala Val Cys Lys Glu Lys Ile Gly Trp Arg Lys Asp Ala Leu His Leu
260 265 270

Leu Val Phe Thr Thr Asp Asp Val Pro His Ile Ala Leu Asp Gly Lys
275 280 285

Leu Gly Gly Leu Val Gln Pro His Asp Gly Gln Cys His Leu Asn Glu
290 295 300

Ala Asn Glu Tyr Thr Ala Ser Asn Gln Met Asp Tyr Pro Ser Leu Ala
305 310 315 320

Leu Leu Gly Glu Lys Leu Ala Glu Asn Asn Ile Asn Leu Ile Phe Ala
325 330 335

Val Thr Lys Asn His Tyr Met Leu Tyr Lys Asn Phe Thr Ala Leu Ile
340 345 350

Pro Gly Thr Thr Val Glu Ile Leu Asp Gly Asp Ser Lys Asn Ile Ile
355 360 365

Gln Leu Ile Ile Asn Ala Tyr Asn Ser Ile Arg Ser Lys Val Glu Leu

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370	375	380
Ser Val Trp Asp Gln Pro Glu Asp Leu Asn Leu Phe Phe Thr Ala Thr		
385	390	395 400
Cys Gln Asp Gly Val Ser Tyr Pro Gly Gln Arg Lys Cys Glu Gly Leu		
	405	410 415
Lys Ile Gly Asp Thr Ala Ser Phe Glu Val Ser Leu Glu Ala Arg Ser		
	420	425 430
Cys Pro Ser Arg His Thr Glu His Val Phe Ala Leu Arg Pro Val Gly		
	435	440 445
Phe Arg Asp Ser Leu Glu Val Gly Val Thr Tyr Asn Cys Thr Cys Gly		
	450	455 460
Cys Ser Val Gly Leu Glu Pro Asn Ser Ala Arg Cys Asn Gly Ser Gly		
465	470	475 480
Thr Tyr Val Cys Gly Leu Cys Glu Cys Ser Pro Gly Tyr Leu Gly Thr		
	485	490 495
Arg Cys Glu Cys Gln Asp Gly Glu Asn Gln Ser Val Tyr Gln Asn Leu		
	500	505 510
Cys Arg Glu Ala Glu Gly Lys Pro Leu Cys Ser Gly Arg Gly Asp Cys		
	515	520 525
Ser Cys Asn Gln Cys Ser Cys Phe Glu Ser Glu Phe Gly Lys Ile Tyr		
	530	535 540
Gly Pro Phe Cys Glu Cys Asp Asn Phe Ser Cys Ala Arg Asn Lys Gly		
545	550	555 560
Val Leu Cys Ser Gly His Gly Glu Cys His Cys Gly Glu Cys Lys Cys		
	565	570 575
His Ala Gly Tyr Ile Gly Asp Asn Cys Asn Cys Ser Thr Asp Ile Ser		
	580	585 590
Thr Cys Arg Gly Arg Asp Gly Gln Ile Cys Ser Glu Arg Gly His Cys		
	595	600 605

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Leu Cys Gly Gln Cys Gln Cys Thr Glu Pro Gly Ala Phe Gly Glu Met
610 615 620

Cys Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Ser Thr Lys Arg Asp
625 630 635 640

Cys Val Glu Cys Leu Leu Leu His Ser Gly Lys Pro Asp Asn Gln Thr
645 650 655

Cys His Ser Leu Cys Arg Asp Glu Val Ile Thr Trp Val Asp Thr Ile
660 665 670

Val Lys Asp Asp Gln Glu Ala Val Leu Cys Phe Tyr Lys Thr Ala Lys
675 680 685

Asp Cys Val Met Met Phe Thr Tyr Val Glu Leu Pro Ser Gly Lys Ser
690 695 700

Asn Leu Thr Val Leu Arg Glu Pro Glu Cys Gly Asn Thr Pro Asn Ala
705 710 715 720

Met Thr Ile Leu Leu Ala Val Val Gly Ser Ile Leu Leu Val Gly Leu
725 730 735

Ala Leu Leu Ala Ile Trp Lys Leu Leu Val Thr Ile His Asp Arg Arg
740 745 750

Glu Phe Ala Lys Phe Gln Ser Glu Arg Ser Arg Ala Arg Tyr Glu Met
755 760 765

Ala Ser Asn Pro Leu Tyr Arg Lys Pro Ile Ser Thr His Thr Val Asp
770 775 780

Phe Thr Phe Asn Lys Phe Asn Lys Ser Tyr Asn Gly Thr Val Asp
785 790 795 --

Claim 1, Column 79, line 25, delete "or" and insert --and--.

With the above correction, Claim 1 reads:

1. An isolated nucleic acid encoding an isolated mammalian anti-dual integrin antibody comprising (i) all of the heavy chain CDR amino acid sequences of SEQ ID NOS:1, 2, and 3; and (ii) all of the light chain CDR amino acids sequences of SEQ ID NOS:4, 5, and 6.

Claim 3, Column 79, line 29, insert --vector-- between “acid” and “according”.

With the above correction, Claim 3 reads:

3. A prokaryotic or eukaryotic host cell comprising an isolated nucleic acid vector according to claim 2.

Claim 9, Column 80, line 26, delete “293,” before “HeLa”.

With the above correction, Claim 9 reads:

9. A host cell according to claim 8, wherein said host cell is at least one selected from COS-1, COS-7, HEK293, BHK21, CHO, BSC-1, Hep G2, P3X63Ag8.653, SP2/0, HeLa, myeloma, or lymphoma cells.